## Appendix I Alignment of instant SEO ID NO: 1 and BAA23691.2 (KIAA0395)

Man | BAA23691.2 | KIAA0395 [Homo sapiens] Length=879 Score = 1829 bits (4738), Expect = 0.0, Method: Compositional matrix adjust. Identities = 878/879 (99%), Positives = 878/879 (99%), Gaps = 0/879 (0%) SCKYCDFRSHDWTOFVGHMNSEHTDFNKDPTFVCSGCSFLAKTPEGLSLHNATCHSGEAS 137 Ouerv SCKYCDFRSHDMTQFVGHMNSEHTDFNKDPTFVCSGCSFLAKTPEGLSLHNATCHSGEAS SCKYCDFPSHDMTQFVGHMRSEHTDFNKDFTFVCSGCSFLAFTPEGLSLHBATCHSGEAS Shict 1 Query 138 FVMNVAKPDNHVVVEOSTPRSTSTPDLAGEPSARGADGOARTITTKTPIMKTMKGKARAK FVWNVAKPDWHVVVEQSIPESTSTPDLAGEPSAEGADGQAEIIITKTFIMKIMKGKAEAK Shict 6.1 PVWNVAKPDRHVVVEQSIPESTSTPDLAGEPSAEGADGQAEIIITETPIMKIMKGKABAK Query KIHTLKERVPSOPVGEALPKLSTGEMEVREGDHSFINGAVPVSOASASSAKRPHAANGPL KIHTLKE NVPSQPVGEALFKLSTGEMEVREGDHSPIHGAVPVSQASASSAKNFHAANGPL 121 KIHTLKENVF3OPVGEALPKLSTGEMEVPEGDHSFIRGAVPVSQASASSAKNPHAANGFL 180 258 IGTVPVLPAGIAOFLSLOOOPFVHAOHHVHOFLFTAKALPKVMIPLSSIPTYNAAMDSNS Query IGTVPVLPAGIAOFLSLOOOPFVHAOHHVHOPLPTAKALPKVMIPLSSIPTYNAAMDSNS 181 IGTVPVLPAGIAQFLSLQQQPFVHAQHHVHQPLPTAKALPKVMIPLSSIPTYNAAMDSNS 240 Shjet Query 318 FLKRSPHKFPYPTKAELCYLTVVTKYPEEQLKIWPTAQRLKQGISWSPEEIEDARKKMFW PLKWSPHKPPYPTKAELCYLTVVTKYPEEQLKIWPTAQRLKQGISWSPEEIEDARKKMPN Sbjet 241 FLKMSPHKFPYPTKAELCYLTVVTKYPEEQLKIWFTAQPLKQGISWSPEEIEDARKKMFN 300 378 TVIQNVPQPTITVLBTPLVASAGEVQHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ 437 Query TVIQ5VFQFTITVLNTFLVASAGNVQHLIQAALFGHVVGQFEGTGGGLLVTQFLMANGLQ Shirt 301 TVIOSVPOPTITVLNTPLVASAGNVOHLIQAALPGHVVGQPEGTGGGLLVTQPLMANGLQ 360 Overv 438 ATSSPLPLTVTSVPKQPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSITSQAFLDASIY ATSSPLELTVTSVPKOPGVAPIRTVCSNTTSAVKVVNAAOSLLTACPSITSOAFLDASIY 361 ATSSPLFLTVTSVPKOPGVAPINTVCSNTTSAVKVVNAAOSLLTACPSITSOAPLDASIY 42 ft 498 KNKKSHE OLSALKGSFCRNOFPGOSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLKGSRA 557 KNKKSHEOLSALKGSFCRNOFFGOSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLKGSRA Sbict 421 KNKKSHEOLSALKGSFCRNOFPGOSEVEHLTKVTGLSTREVRKMFSDRRYHCRNLKGSRA 480 558 MIPGDRSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATRPSAKRQSWHQTPDFTPTKYK Query MIPGDHSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATHPSAKROSWHOTPDFTPTKYK Shact 481 MIPGDHSSIIIDSVPEVSFSPSSKVPEVTCIPTTATLATHPSAKRQSWRQTPDFTPTKYK 540 618 BRAPEQLRALESSFAQNPLPLDEELDRLRSETKMTRREIDSWESERRKKVNAEETKKAEE 677 Query EPAPEQLRALESSFAQNFLPLDEELDRLRSETKMTRREIDSWFSERRKKVNAEETKKAEE Sbact 541 ERAPECTRALESSPAONPLPT/DEFLORITSETKMTRREIDSWESERRKKVRAHETKKAER 600 678 NASQEEEEAAEDEGGEEDLASELRVSGENGSLEMPSSHILAERKVSPIKIELKNLFVTEA Onerv MASCEEEEAAEDEGGEEDLASELRVSGEWGSLEMPSSHILAERKVSPIKINLKNLRVTEA 601 RASCEEEEAAEDEGGEEDLASELPVSGENGSLEMPSSHILAERKVSPIKINLKNLKVTEA Sbact NGRWEIPGLGACDPEDDESNKLAHOLPGKVSCKKTAOORHLLPGLFVOTGWPSNODYD31 Ouerv ngpneipglgacdpeddesnklaeqlpgkvsckktaqqrhllrqlfvqtqwpsnqdydsi Sbact 661 NGRNEIPGLGACDPEDDESNKLAEOLPGKVSCKKTAOORHLLROLFVOTGMPSNODYDSI 720 Query 798 MAQTGLF RPEVVRMFGDSRYALKNGQLKWYED YKRGNFF PGLLV I APGNRELLQD YYMTH 857 MACTGLERPEVVRMFGDSRYALKNGOLKMYEDYKRGNFFPGLLVTAPGNRELLODYYMTH Sbjet 721 MAQTGLPRPEVVRWFGDSRYALKNGQLKWYEDYKRGNPFPGLLVIAPGNRELLQDYYMTH 780 Query 858 KMLYEEDLQNLCDKTQM3SQQVKQWPAENMGEETRAVADTG3EDQGPGTGELTAVHKGNG 917 KMLYEEDLQNLCDKTQMSSQQVKQWFAEKMGEETRAVADTGSEDQGPGT ELTAVHKGMG 781 KMLYEEDLONLCDKTONSSQOVKOWFAEKMGEETRAVADTGSEDQGPGTTELTAVHKGMG 840 Shict Query 918 DTYSEVSENSESWEPRVPEASSEPFDTSSPOAGROLETD 956

DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD 3bjct 841 DTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD 879